SEQUENCE LISTING

<110> Ballinger, Marcus

<120> Constructs for Homogenously Processed Preparations of Beta Site App-Cleaving Enzyme

<130> 2004345-0021

<140> 10/726,967
<141> 2003-12-02

<160> 110

<170> PatentIn version 3.2

<210> 1
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Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
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Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
    50                  55                  60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65                  70                  75                  80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
                85                  90                  95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
            100                 105                 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
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Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
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Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
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145                 150                 155                 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
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Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
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Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
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Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
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Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225                 230                 235                 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
                245                 250                 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
            260                 265                 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
        275                 280                 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
    290                 295                 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305                 310                 315                 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
                325                 330                 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
            340                 345                 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
        355                 360                 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
    370                 375                 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385                 390                 395                 400
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Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
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Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
485 490 495

Ile Ser Leu Leu Lys
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Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
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<223> Residues 22-37 of human BACE1 preprosequence

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Glu Asn Leu Tyr Phe Asn Ala
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Pro Gly Ala Ala His Tyr Ala
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Asp Asp Asp Asp Lys
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Asp Glu Asp Asp Lys
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Asp Asp Glu Asp Lys
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Glu Asp Asp Asp Lys
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Glu Glu Glu Glu Lys
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Ile Glu Xaa Asp Xaa Gly
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Ile Glu Xaa Asp Xaa Ala
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Ile Met Xaa Asp Xaa Gly
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<210> 42
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Val Glu Xaa Asp Xaa Gly
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1 5

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Val Met Xaa Asp Xaa Ala
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Val Gln Xaa Asp Xaa Gly
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Val Gln Xaa Asp Xaa Ala
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Val Arg His Gln Ser
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Ile Glu Gly Arg
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<220>

<223> Residues 74-101 of human BACE1 preprosequence

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Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn
1 5 10 15

Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
20 25

<210> 53
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<223> Residues 118-145 of human BACE1 preprosequence

<400> 53

Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr
1 5 10 15

Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu
20 25

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<223> Residues 165-185 of Human BACE1 Preprosequence isoforms A and B

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Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
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Gly Leu Ala Tyr Ala
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Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu
1 5 10 15

Arg Leu Pro

<210> 56
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Glu Leu Asn Leu Glu Thr Asp
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<210> 57
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Glu Ile Asn Leu Glu Thr Asp
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<210> 58
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Glu Ile Asn Phe Glu Thr Asp
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<210> 59
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Glu Val Asn Leu Asp Ala Glu
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<210> 61
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Glu Ile Asn Phe Gln Phe Val Asp
1 5

<210> 62
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<212> PRT
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Glu Ile Asn Phe Ser Ala Ser Phe
1 5

<210> 63
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Glu Pro Gly Arg Arg Gly
1 5

<210> 64
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<212> DNA
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<220>
<223> Primer used to obtain bases 126-374 of human BACE1, and bases 126-1362 of human BACE1

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gctgccccgg gagaccgacg aaga 24

<210> 65
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<212> DNA
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<220>
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cggaggtccc ggtatgtgct ggac 24

<210> 66
<211> 24
<212> DNA
<213> Artificial

<220>
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ccagaggcag ctgtccagca cata 24

<210> 67
<211> 24
<212> DNA
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<220>
<223> Primer used to obtain nucleotides 339-770 of human BACE1

<400> 67
tcccgccgga tgggtgtata ccag 24

<210> 68
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Primer used to obtain nucleotides 735-1551 of human BACE1

<400> 68
gtacacaggc agtctctggt atacacc 27

<210> 69
<211> 29
<212> DNA
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<220>
<223> Primer used to obtain nucleotides 735-1551 of human BACE1

<400> 69
gtgtggtcca ggggaatctc tatcttctg 29

<210> 70

<211> 40
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<220>
<223> Primer containing an XhoI restriction site used to obtain nucleotides 126-1551 of human BACE1

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gtcatcgtct cgagtcactt cagcagggag atgtcatcag 40

<210> 71
<211> 60
<212> DNA
<213> Artificial

<220>
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<400> 71
cggctgcccc tgcgcagcgg cctgggggggc gccccccctgg ggctgcggct gccccgggag 60

<210> 72
<211> 60
<212> DNA
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<223> Forward primer used to extend nucleotides 126-1362 of human BACE1 in 5' direction

<400> 72
atgggcgcgg gagtgctgcc tgcccacggc acccagcacg gcatccggct gcccctgcgc 60

<210> 73
<211> 57
<212> DNA
<213> Artificial

<220>
<223> Foward primer containing an EcoR1 restriction site used to extend nucleotides 126-1362 of human BACE1 in 5' direction

<400> 73
ccggaattca tggcccaagc cctgccctgg ctcctgctgt ggatgggcgc gggagtg 57

<210> 74
<211> 33
<212> DNA
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<220>
<223> Forward primer containing an NdeI restriction site used to obtain bases 1-1362 of human BACE1

<400> 74
cgccatatgg cgggagtgct gcctgcccac ggc 33

<210> 75
<211> 36
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<223> Reverse primer containing an EcoRI restriction site used to obtain bases 1-1362 of human BACE1

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ccggaattct caggttgact catctgtctg tggaat 36

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Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
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Pro Leu Gly Leu Arg Leu Pro Arg Leu Val Pro Arg Gly Ser Glu Thr
20 25 30

Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met
35 40 45

Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met
50 55 60

Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly
65 70 75 80

Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg
85 90 95

Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly
100 105 110

Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr
115 120 125

Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn
130 135 140

Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn
145 150 155 160

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Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp
                165                 170                 175

Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val
            180                 185                 190

Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn
        195                 200                 205

Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly
    210                 215                 220

Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg
225                 230                 235                 240

Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly
                245                 250                 255

Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile
            260                 265                 270

Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu
        275                 280                 285

Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro
    290                 295                 300

Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr
305                 310                 315                 320

Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu
                325                 330                 335

Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu
            340                 345                 350

Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe
        355                 360                 365

Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met
    370                 375                 380

Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe
385                 390                 395                 400

Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val
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405 410 415

Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile
420 425 430

Pro Gln Thr Asp Glu Ser Thr
435

<210> 77
<211> 48
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for insertion of thrombin cleavage site into soluble human proBACE1

<400> 77
ctcttcgtcg gtctcagaac cacgcggaac cagacgtggc agacgcag 48

<210> 78
<211> 433
<212> PRT
<213> Artificial

<220>
<223> Soluble human proBACE1 containing an engineered RLPL site starting at position 21

<400> 78

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
1 5 10 15

Pro Leu Gly Leu Arg Leu Pro Leu Glu Thr Asp Glu Glu Pro Glu Glu
20 25 30

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly
35 40 45

Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro
50 55 60

Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
65 70 75 80

Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu
85 90 95

Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr
100 105 110

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Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro
        115                 120                 125

His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu
    130                 135                 140

Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly
145                 150                 155                 160

Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe
                165                 170                 175

Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu
            180                 185                 190

Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala
        195                 200                 205

Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr
    210                 215                 220

Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu
225                 230                 235                 240

Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp
                245                 250                 255

Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr
            260                 265                 270

Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile
        275                 280                 285

Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
    290                 295                 300

Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
305                 310                 315                 320

Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
                325                 330                 335

Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
            340                 345                 350

Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
        355                 360                 365
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Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
370 375 380

Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
385 390 395 400

Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
405 410 415

Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
420 425 430

Thr

<210> 79
<211> 7
<212> PRT
<213> Artificial

<220>
<223> RLPL site

<400> 79

Arg Leu Pro Leu Glu Thr Asp
1 5

<210> 80
<211> 42
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide to introduce RLPL site into soluble human proBACE1

<400> 80
ctcttcgtcg gtctccagtg gcagacgcag acccagtgga gc 42

<210> 81
<211> 433
<212> PRT
<213> Artificial

<220>
<223> Soluble human proBACE1

<400> 81

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
1 5 10 15

Pro Leu Gly Leu Glu Leu Asn Leu Glu Thr Asp Glu Glu Pro Glu Glu

20 25 30

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly
35 40 45

Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro
50 55 60

Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
65 70 75 80

Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu
85 90 95

Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr
100 105 110

Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro
115 120 125

His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu
130 135 140

Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly
145 150 155 160

Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe
165 170 175

Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu
180 185 190

Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala
195 200 205

Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr
210 215 220

Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu
225 230 235 240

Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp
245 250 255

Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr
260 265 270

Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile
275 280 285

Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
290 295 300

Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
305 310 315 320

Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
325 330 335

Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
340 345 350

Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
355 360 365

Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
370 375 380

Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
385 390 395 400

Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
405 410 415

Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
420 425 430

Thr

<210> 82
<211> 42
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide to introduce ELNL site into soluble human proBACE1

<400> 82
ctcttcgtcg gtctccaggt tcagttccag acccagtgga gc 42

<210> 83
<211> 27
<212> DNA
<213> Artificial

<220>

<223> Oligonucleotide to introduce EINL site into soluble human proBACE1

<400> 83
ggtctccagg ttgatttcca gacccag 27

<210> 84
<211> 433
<212> PRT
<213> Artificial

<220>
<223> Soluble human proBACE1 containing an engineered EINL site starting at position 21

<400> 84

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
1 5 10 15

Pro Leu Gly Leu Glu Ile Asn Leu Glu Thr Asp Glu Glu Pro Glu Glu
20 25 30

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly
35 40 45

Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro
50 55 60

Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
65 70 75 80

Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu
85 90 95

Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr
100 105 110

Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro
115 120 125

His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu
130 135 140

Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly
145 150 155 160

Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe
165 170 175

Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu

180 185 190

Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala
195 200 205

Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr
210 215 220

Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu
225 230 235 240

Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp
245 250 255

Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr
260 265 270

Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile
275 280 285

Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
290 295 300

Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
305 310 315 320

Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
325 330 335

Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
340 345 350

Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
355 360 365

Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
370 375 380

Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
385 390 395 400

Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
405 410 415

Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
420 425 430

Thr

<210> 85
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for L91C mutatio of human BACE1

<400> 85
gcctgtatcc acacagatgt tgagcgt 27

<210> 86
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for D93C mutation of human BACE1

<400> 86
actgctgcct gtacacacca ggatgtt 27

<210> 87
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for T133C mutation of human BACE1

<400> 87
ttcccacttg ccacaggtgt agggcac 27

<210> 88
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for Q134C mutation of human BACE1

<400> 88
ttcccacttg ccacaggtgt agggcac 27

<210> 89
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for K168C mutation of human BACE1

<400> 89
gttgatgaag aaacagtctg attcagt 27

<210> 90
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for F169C mutation of human BACE1

<400> 90
gccgttgatg aaacacttgt ctgattc 27

<210> 91
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for I171C mutation of human BACE1

<400> 91
gttggagccg ttacagaaga acttgtc 27

<210> 92
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for W176C mutation of human BACE1

<400> 92
caggatgcct tcacagttgg agccgtt 27

<210> 93
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for I179C mutation of human BACE1

<400> 93
ggccagcccc agacagcctt cccagtt 27

<210> 94
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for I187C mutation of human BACE1

<400> 94
gtcaggcctg gcacactcag cataggc 27

<210> 95
<211> 27

<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for R189C mutation of human BACE1

<400> 95
ggagtcgtca ggacaggcaa tctcagc 27

<210> 96
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for Y259C mutation of human BACE1

<400> 96
gatcacctca taacaccact cccgccg 27

<210> 97
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for K285C mutation of human BACE1

<400> 97
gtccacaatg ctacagtcat agttgta 27

<210> 98
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for I287C mutation of human BACE1

<400> 98
gccactgtcc acacagctct tgtcata 27

<210> 99
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for D289C mutation of human BACE1

<400> 99
ggtggtgcca ctacacacaa tgctctt 27

<210> 100
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for T292C mutation of human BACE1

<400> 100
acgaaggttg gtacagccac tgtccac 27

<210> 101
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for N294C mutation of human BACE1

<400> 101
gggcaaacga agacaggtgg tgccact 27

<210> 102
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for R296C mutation of human BACE1

<400> 102
tttcttgggc aaacaaaggt tggtggt 27

<210> 103
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for G325C mutation of human BACE1

<400> 103
caccagctgc tccactagcc agaaacc 27

<210> 104
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for R368C mutation of human BACE1

<400> 104
atcttccact ggacacaggt attgctg 27

<210> 105
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for K382C mutation of human BACE1

<400> 105
tgagatggca aaacagtaac agtcgtc 27

<210> 106
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for S386C mutation of human BACE1

<400> 106
cgtggatgac tgacagatgg caaactt 27

<210> 107
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for T390C mutation of human BACE1

<400> 107
cataacagtg ccacaggatg actgtga 27

<210> 108
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for V393C mutation of human BACE1

<400> 108
cagctcccat acaagtgccc gtggatg 27

<210> 109
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for inactivating D90N mutation of human BACE1

<400> 109
actgctgcct gtgttcacca ggatgtt 27

<210> 110
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide for inactivating D289N mutation of human BACE1

<400> 110
ggtggtgcca ctgttcacaa tgctctt 27